

FIGURE 3

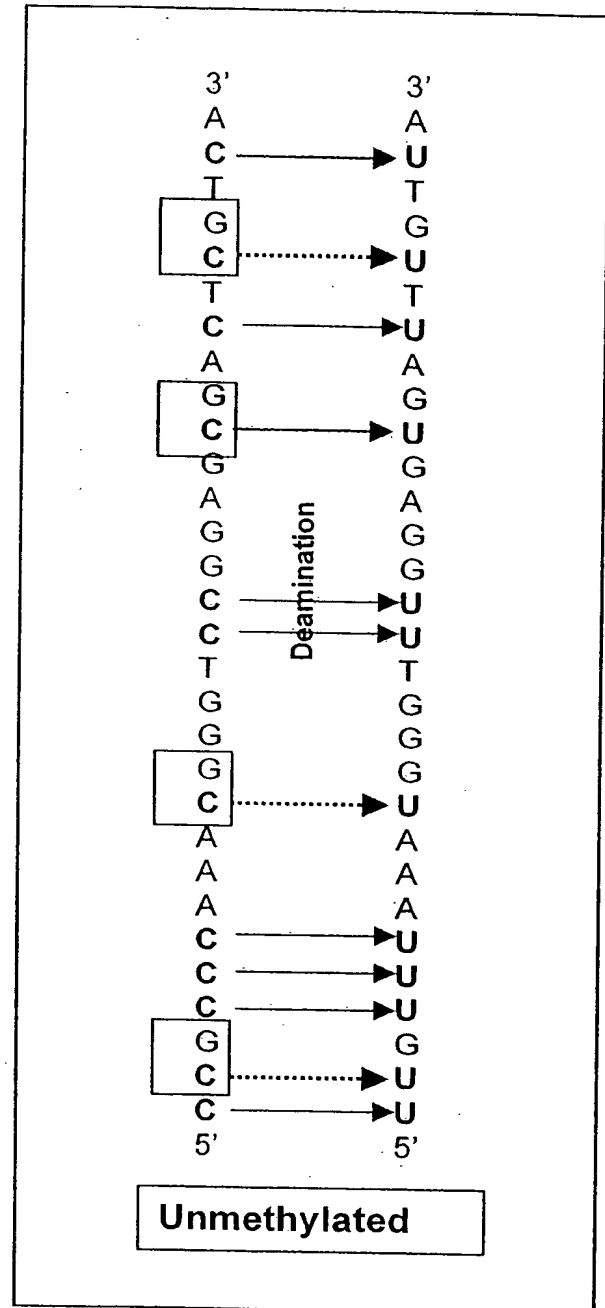
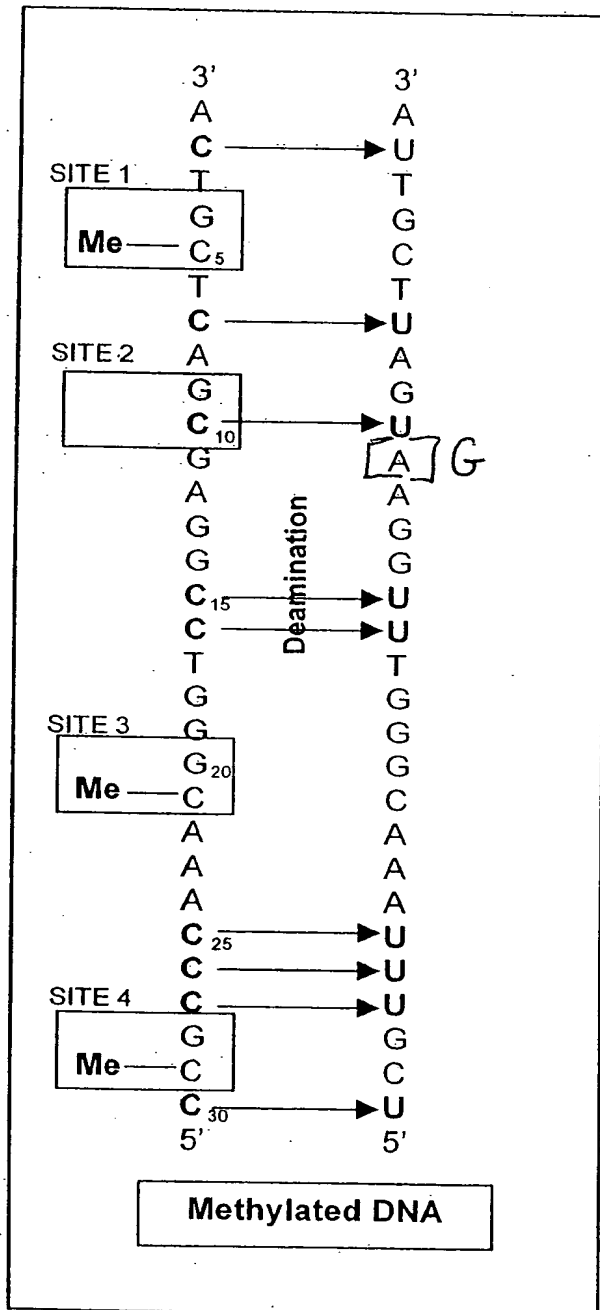


FIGURE 13

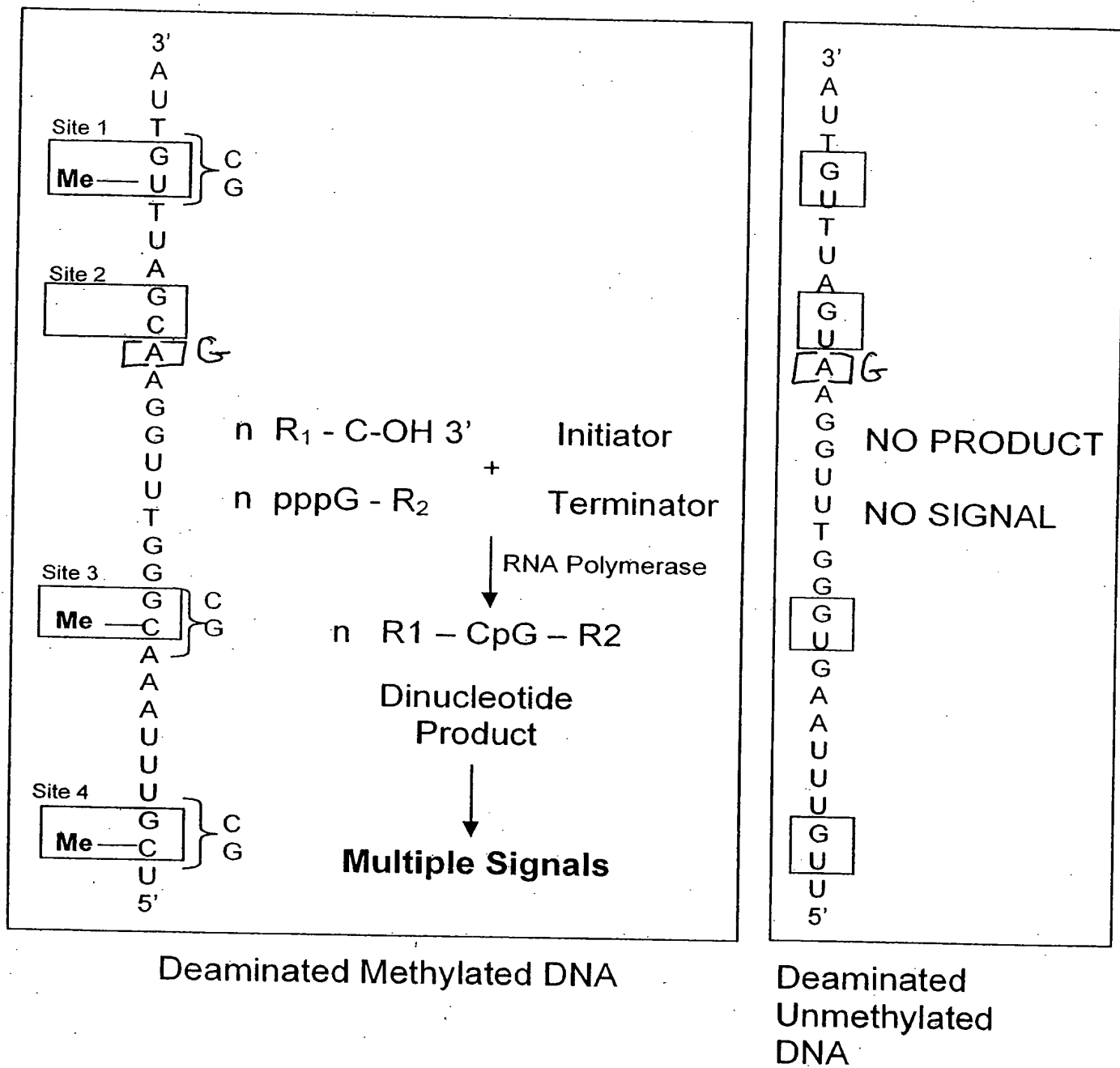
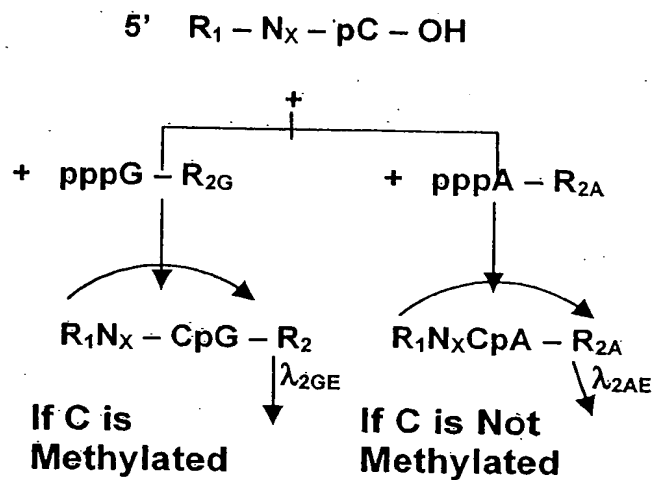
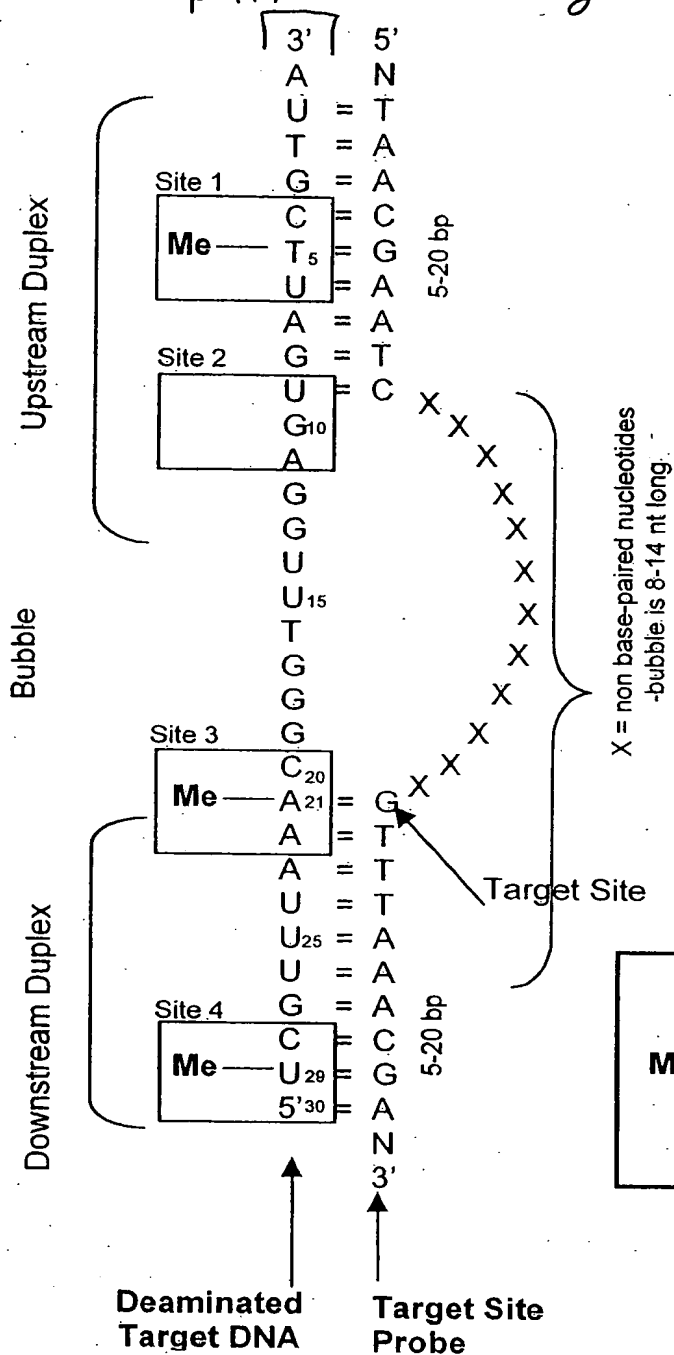


FIGURE 14

entire strand move down
1 nucleotide so that bases
pair correctly



- M = 1 If both copies are 100% methylated: Only λ_{2GE} detected
- M = 0.5 If 1 copy is methylated: Both λ_{2GE} and λ_{2AE} detected
- M = 0 If both copies unmethylated: only λ_{2AE} detected

$$M = \text{Methylation Index} = \frac{E\lambda_{2GE}}{E\lambda_{2GE} + E\lambda_{2GA}}$$

FIGURE 15

AGGCAGATTAAGCATGTGCTTAAGGCATCAGCAAAGTCTGAGCAATCCATTTTTTAAACGCTAGTACATGTTTT
TGATAAGCTTAAAAAGTAGTAGTCACAGGAAAAATTAGAACTTTTACCTCCTTGCGCTTGTTATACTCTTTAGT
GCTGTTTAACTTTTCTTTGTAAGTGAGGGTGGTGGAGGGTGCCCATATCTTTTCAGGGAGTAAGTCTTCTT
GGTCTTTCTTTCTTTCTTTCTTTCTTTTCTTTGAGACCAAGTTTCGCTCTTGCTCTCCAGGCTGGAGTGCAA
TGCGCGCATCTCGGCTCACTGCAACCTCCGCCTTCTCCTGGGTTCAAGCGATTCTCCTACATCAGCCTCCGA
GTAGCTGGGATTACAGGCTGCGCCACCAAGCCCCGCTAATTTTGTATTTTTTAGTAGAGACAGGGTTTCGC
CATGTTGGTCAGGCTTGTCTCGAACTCCTGGCCTCAGGTGATCCGCCTGTCTCGGCCTCCAGAAATGCTGG
GATTATAGACGTGAGCCACCGCATCGGACTTTCTTTATGTAAATAGTATAATTCTATCCAAAGCATTTTTT
TTTTTTTTGAGTCGGAGTCTCATTCTGTCAACCAGGCTGGAGGGTGGTGGCGCATCTCGGCTTACTGCAA
CCTCTGCCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGAATTACACAGCTGCGCCA
CCATGGCCAGCTAATTTTTGTATTTTTAGTAGAGACGGGGTGTCAACATTTTGGCCAAGCTGGCCTCGAACTC
CTGACCTCAGGTGATCTGCCCCGCTCGGCTTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCGCGTCTCT
GCTCCAAAGCATTTTTCTTTCTATGCCTCAAAACAAGATTGCAAGCCAGTCTCAAAGCGGATAATTCAAGAGC
TAACAGGTATTAGCTTAGGATGTGTGGCACTGTTCTTAAGGCTTATATGTATTAATACATCATTTAAACTCACA
ACAAACCCATATAAAGCAGGGGGGCACTCATATCCCTTCCCCCTTTATAATTACGAAAAATGCAAGGTATTTTC
AGTAGAAAGAGAAATGTGAGAAGTGTGAAGGAGACAGGACAGTATTTGAAGCTGGTCTTTGGATCACTGTG
CAACTCGCTTCTAGAACACTGAGCACTTTTTCTGGTCTAGGAATTTAGACTTTGAGAATGGAGTCCGTCCTT
CCAATGACTCCCTCCCCATTTTCTATGTCTGCTACAGCGAGAATCTCCCCGTCCGTATTAATAAACCTCA
TCTTTTCAAGTCTGCTCTTATACCAGGCAATGTACACGCTGTGAGAAACCTTGGCCAGACAGCCGTTTTAC
ACGACAGGAGGGGAAGGGGAGGGGAAGGAGAGAGCAGTCCGACTCTCCAAAGGAATCCTTTGAAGTAGGG
TTTCTGACTTAGTGAACCCCGCGCTCCTGAAAATCAAGGGTTGAGGGGGTAGGGGGACACTTTCTAGTCGGTA
CAGGTGATTTGATTCTCGGTGGGGCTCTCACAACCTAGGAAAGAATAGTTTTGCTTTTTCTTATGATTAAGA
AGAAGCCATACTTTCCCTATGACACCAAACACCCCGATTCAATTTGGCAGTTAGGAAGGTTGTATCGCGGAG
GAAGGAAACGGGGCGGGGGCGGATTCTTTTTAACAGAGTGAACGCACTCAAACACGCCTTTGCTGGCAGG
CGGGGGAGCGCGGCTGGGAGCAGGGAGGCCGGAGGGCGGTGTGGGGGGCAGGTGGGGAGGAGCCAGT
CTCTCTTCCCTGGCAACGCTGGCTTGGCGAGGGCTGCTTCCGGCTGGTGCCCCCGGGGGAGACCCAACC
TGGGGCGACTTCAGGGGTGCCACATTGCTGAAGTCTCGGAGTTAATAGCACCTCCTCCGAGCACTCGCTC
ACGGCGTCCCCTTGCTTGAAAGATACCGCGGTCCCTCCAGGAGATTGAGGGACAGGGTCTGGAGGGGGC
TCTTCCGCCAGCACCAGGAGGAAGAAAGAGGAGGGGCTGGCTGGTCCAGGAGGGTGGGGCGGACCGCGT
GCGCTCGGCGGCTGCGGAGAGGGGGAGAGCAGGCAGCGGGCGGCGGGGAGCAGCATGGAGCCGCGCGC
GGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCCACGGCCGCGGCCCGGGGTCTGGGTAGAGGAGGT
GCGGGCGCTGCTGGAGGCGGGGGCGCTGCCCAACGCACCGAATAGTTACGGTCTGGAGGCGGATCCAGGT
GGGTAGAGGGTCTGCAGCGGGAGCAGGGGATGGCGGGCGACTCTGGAGGACGAAGTTTGCAGGGGAATT
GGAATCAGGTAGCGCTTCGATTCTCCGAAAAAGGGGAGGCTTCTTGGGGAGTTTTTCAAGGGGTTTGTA
ATACAGACCTCCTCCTGCGACGCCCTGGGGCTTGGGAAGCCAAGGAAGAGGAATGAGGAGCCACGCG
CGTACAGATCTCTCGAATGCTGAGAAGATCTGAAGGGGGGAACATATTTGTATTAGATGGAAGTATGCTCTTT
ATCAGATACAAAATTTACGAACGTTTTGGGATAAAAAGGAGTCTTAAAGAAATGTAAGATGTGCTGGGACTAC
TTAGCCTCCAATTCACAGATACCTGGATGGAGCTTATCTTTCTTACTAGGAGGATTATCAGTGGAATCTGT
GGTGTATGTTGGAATAAATATCGAATATAAATTTTGTATCGAAATTATTCAGAAGCGCGCGCGGCTGCTC
ACGCCTTGTAAATCCCTTCACTTTGGGAGATCAAGGCGGGGGGAATCACCTGAGGTCTGGGAGTTCTGAGACCA
GCCTGGCCAACAGGTGAAACCTCGCCTCTACTAAAAATACAAAAAGTAGCCGGGGGTGGTGGCAGGCGCT
GTAATCCCAGCTACTCGGGAGGTTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCTGAGGTTGTAGTGAAC
AGCGAGATGGAGCCACTTCACTCCAGCCTGGGTGACAGAGTGAGACTTTGTGAAAGAAAGAAAGAGAGAA
AGAGAGAGAGAAAAATTATTCAGAAGCAACTACATATTGTGTTTATTTTTAACTGAGTAGGGCAAATAAATATA
TGTTTGCTGTAGGAACTTAGGAAATAATGAGCCACATTCATGTGATCATTCCAGAGGTAATATGTAGTTACCAT
TTTGGAAATATCTGCTAACATTTTTGCTCTTTTACTATCTTTAGCTTACTTGATATAGTTTATTTGTGATAAGAG
TTTTCAATTCCTCATTTTTGAACAGAGGTGTTTCTCCTCTCCCTACTCCTGTTTTGTGAGGGAGTTAGGGGAG
GATTTAAAGTAATTAATACATGGGTAACCTTAGCATCTCTAAAATTTTGGCAACAGCTTGAACCCGGGAGTTTG
GCTTTGTAGTCTTACAATATCTTAGAAGAGACCTTATTTGTTTAAAAACAAAAGGAAAAAGAAAGTGGATAG
TTTTGACAATTTTTAATGGAG

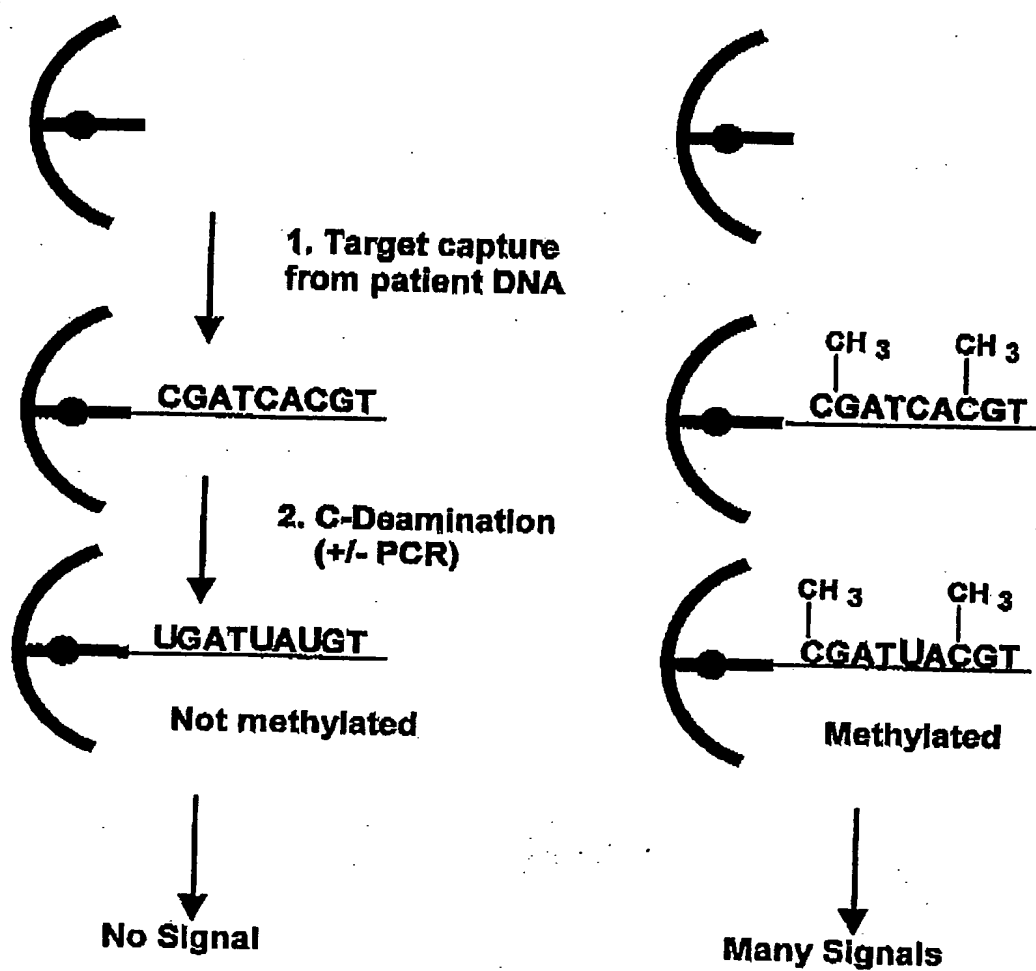


FIGURE 31
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Replacement Sheet

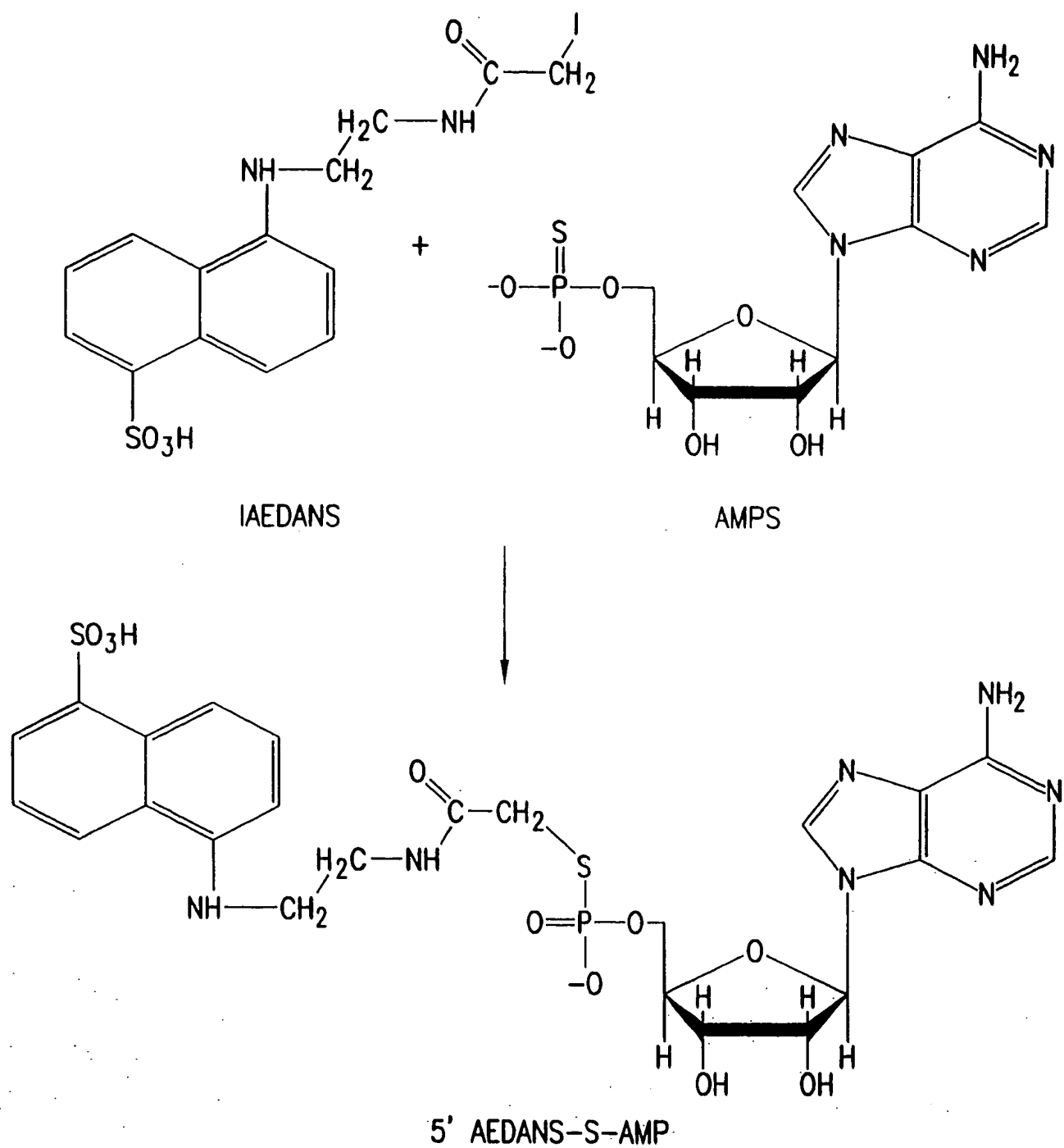


FIG.3

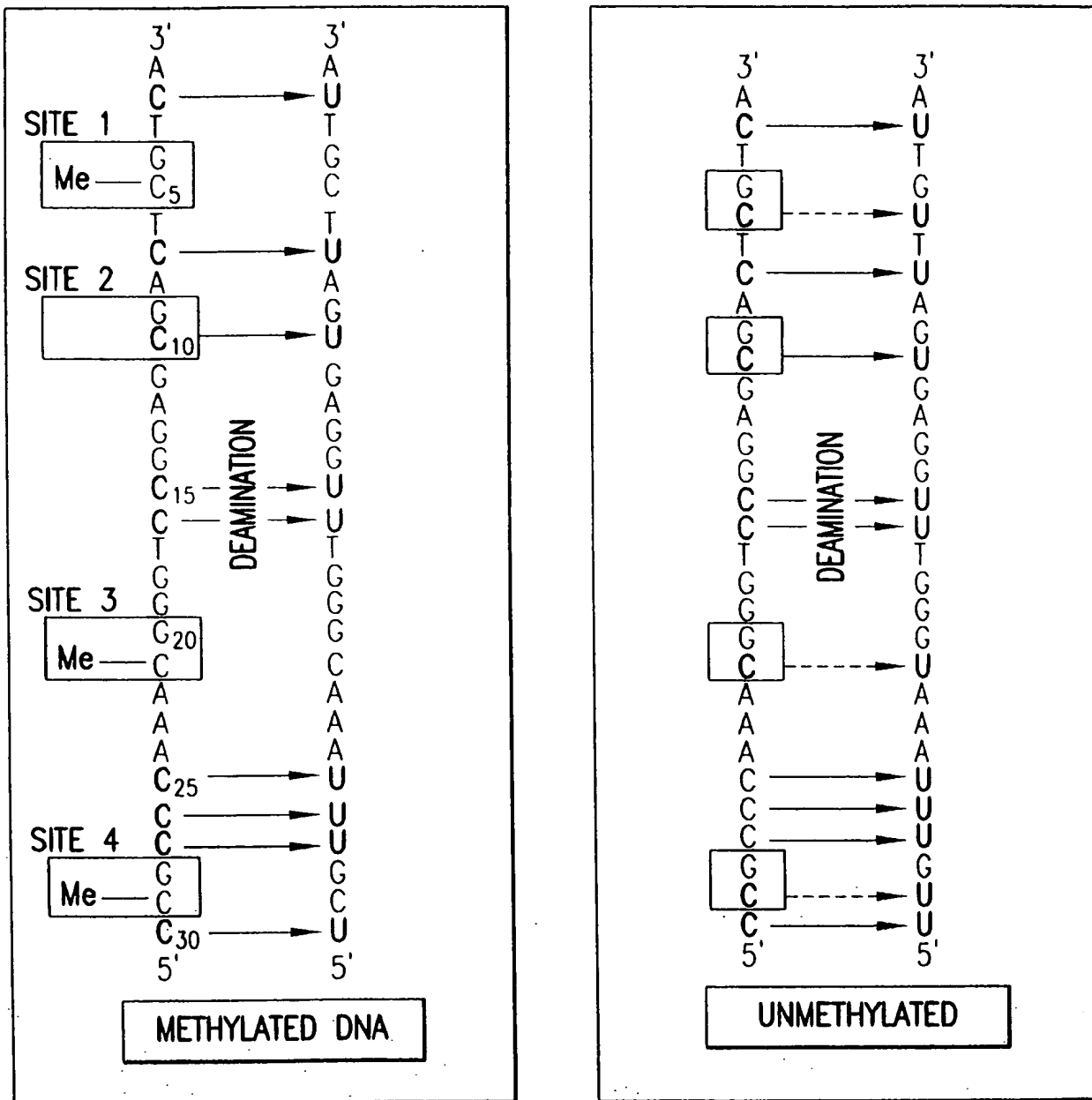


FIG.13

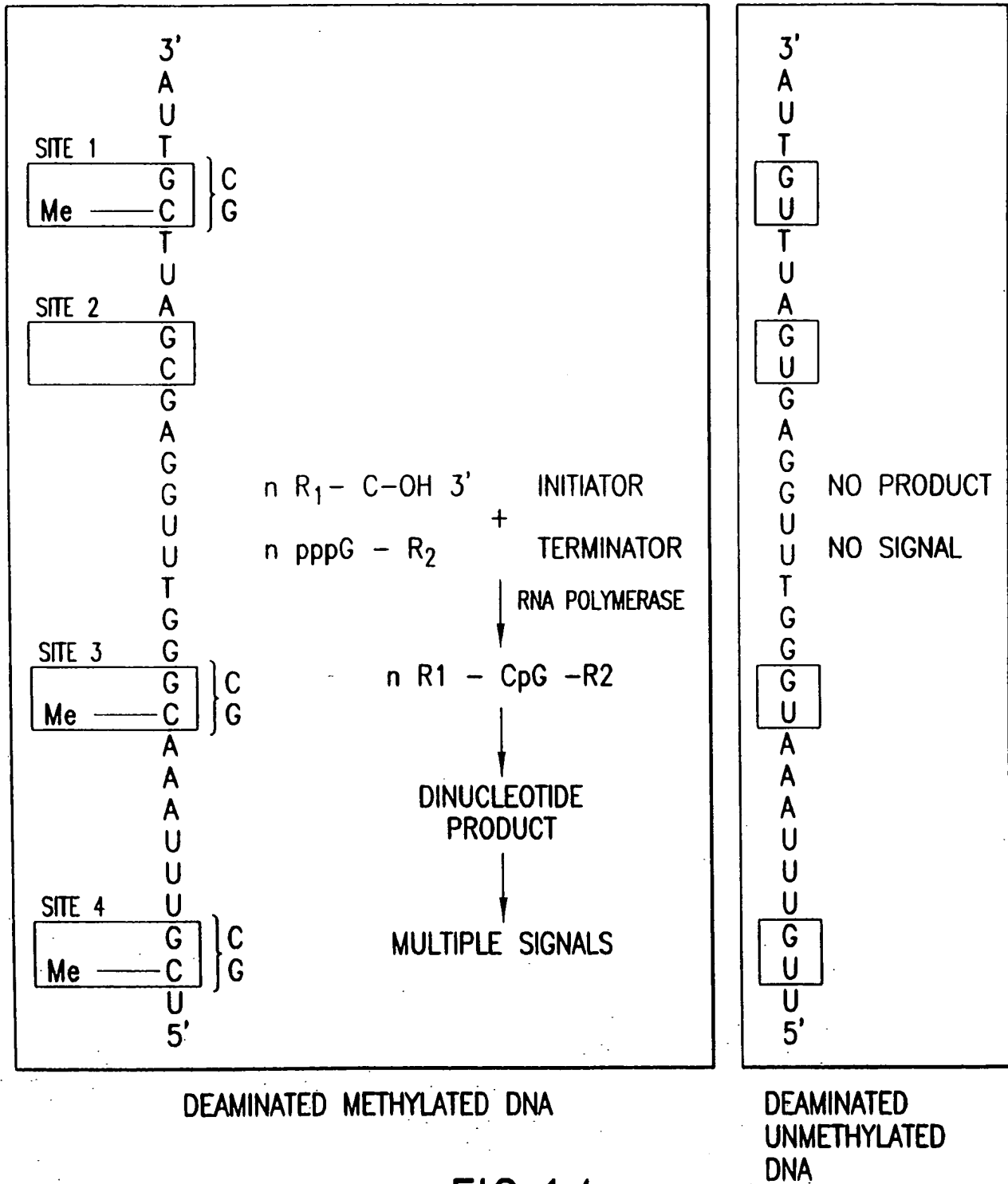


FIG.14

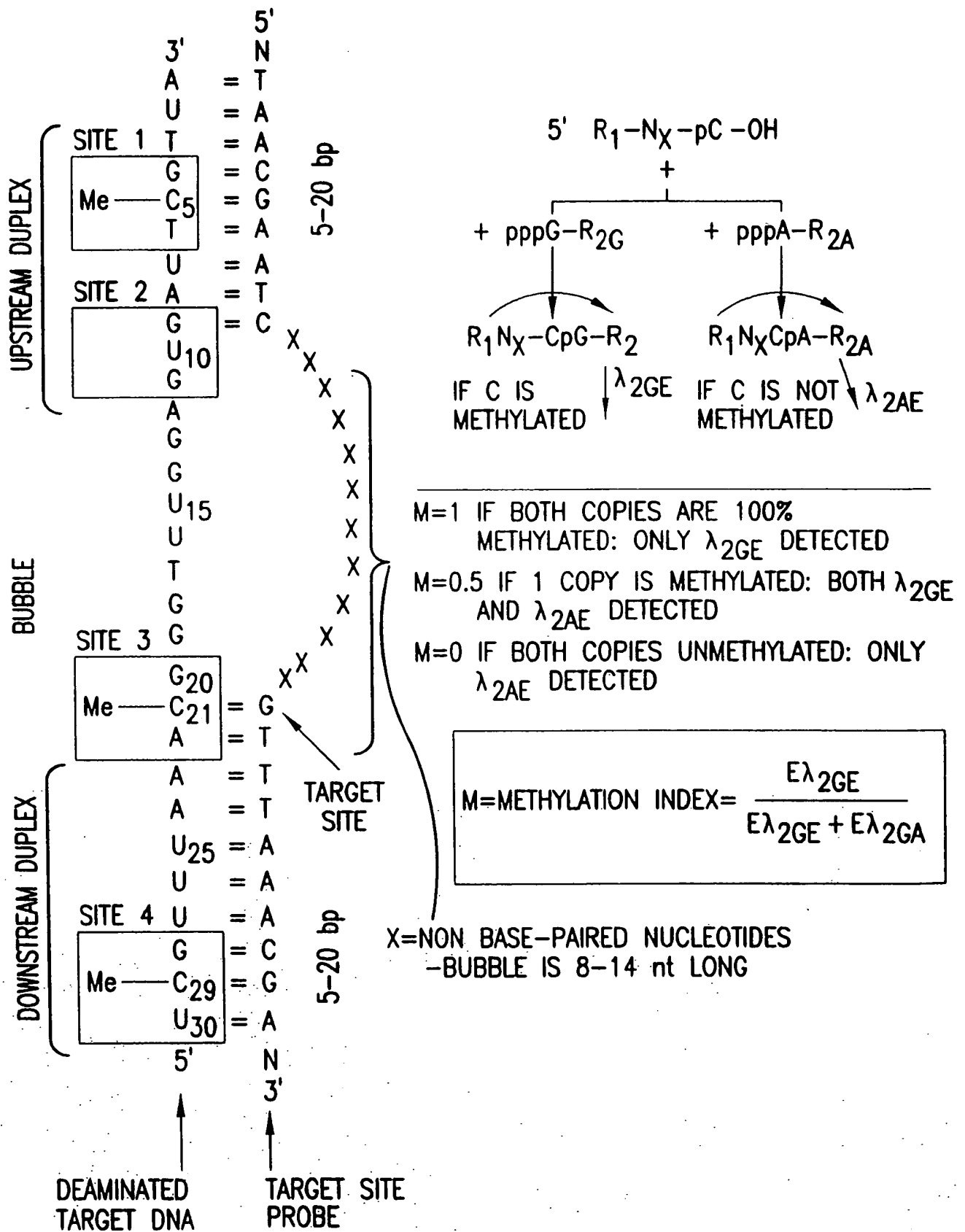


FIG.15

ATATACGGGCTACAAGGTAAAGTCAACCAGGGATTGAATATAACCTTAAACAGAGCTGGATTATCCAGT
AGGCAGATTAAGCATGTGCTTAAGGCATCAGCAAAGCTGAGCAATCCATTTTTTAAACGTAGTACATGTTTT
TGATAAGCTTAAAAAGTAGTAGTCACAGGAAAAATTAGAACTTTTACCTCCTTGCCTTGTATACCTCTTTAGT
GCTGTTAACTTTTCTTTGTAAGTGAGGGTGGTGGAGGGTGCCCATATCTTTTACGGGAGTAAGTTCTTCTT
GGTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTGAGACCAAGTTTCGCTCTTGTCTCCAGGCTGGAGTGCAA
TGGCGCGATCTCGGCTCACTGCAACCTCCGCTTCTCCTGGGTCAAGCGATTCTCCTACATCAGCCTCCGA
GTAGCTGGGATTACAGGCATGCGCCACCAAGCCCCGCTAATTTTGTATTTTGTAGTAGAGACAGGGTTTCGC
CATGTTGGTCAGGCTTGTCTCGAACTCCTGGCCTCAGGTGATCCGCTGTCTCGGCTCCAGAAATGCTGG
GATTATAGACGTGAGCCACCGCATCCGACTTTCTTTTATGTAATAGTGATAATTCTATCCAAAGCATTTTTT
TTTTTTTTGAGTCGGAGTCTATTCTGTCAACCAGGCTGGAGGGTGGTGGCGCGATCTCGGCTTACTGCAA
CCTCTGCCTCCCGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGAATTACACACGTGCGCCA
CCATGGCCAGCTAATTTTGTATTTTGTAGTAGAGACGGGGTGTCAACATTTTGGCCAAGCTGGCCTCGAACTC
CTGACCTCAGGTGATCTGCCCGCTCGGCTTCCCAAAGTGCTGGGATTACAGGTGTGAGCCACCGCGTCT
GCTCCAAAGCATTTTCTTTCTATGCCTCAAAACAAGATTGCAAGCCAGTCTCAAAGCGGATAATTCAAGAGC
TAACAGGTATTAGCTTAGGATGTGTGGCACTGTTCTTAAGGCTTATATGTATTAATACATCATTTAACTCACA
ACAACCCCTATAAAGCAGGGGGCACTCATATTCCCTTCCCCCTTTATAATTACGAAAAATGCAAGGTATTTTC
AGTAGGAAAGAGAAATGTGAGAAGTGTGAAGGAGACAGGACAGTATTTGAAGCTGGTCTTTGGATCACTGTG
CAACTCTGCTTCTAGAACACTGAGCACTTTTCTGGTCTAGGAATTATGACTTTGAGAATGGAGTCCGTCTT
CCAATGACTCCCTCCCCATTTTCTATCTGCCTACAGGCAGAATTCTCCCCGTCCGTATTAAATAAACCTCA
TCTTTTCAGAGTCTGCTTTATACCAGGCAATGTACAGTCTGAGAAACCCTTGCCCCAGACAGCCGTTTTAC
ACGCAGGAGGGGAAGGGGAGGGGAAGGAGAGAGCAGTCCGACTCTCCAAAAGGAATCCTTTGAACTAGGG
TTTCTGACTTAGTGAACCCCGCGCTCCTGAAAATCAAGGGTTGAGGGGGTAGGGGGACACTTTCTAGTCGTA
CAGGTGATTTGATTCTCGGTGGGGCTCTCACAACCTAGGAAAGAATAGTTTTGCTTTTTCTTATGATTAAGAA
AGAAGCCATACTTCCCTATGACACCAAACACCCCGATTCAATTTGGCAGTTAGGAAGGTTGTATCGCGGAG
GAAGGAAACGGGGCGGGGGCGGATTTCTTTTAAACAGAGTGAACGCACTCAAACACGCCTTTGCTGGCAGG
CGGGGAGCGCGGCTGGGAGCAGGGAGGCCGAGGGCGGTGTGGGGGAGGTGGGGAGGAGCCAGT
CCTCCTTCCCTTGCCAACGCTGGCTCTGGCGAGGGCTGCTTCCGGCTGGTGCCCCGGGGGAGACCCAACC
TGGGGCGACTTCAGGGGTGCCACATTGCTAAGTGCTCGGAGTTAATAGCACCTCCTCCGAGCACTCGCTC
ACGGCGTCCCCTTGCTGGAAGATACCGCGGTCCCTCCAGAGGATTTGAGGGACAGGGTCGGAGGGGGC
TCTTCCGCCAGCACCGGAGGAAGAAAGAGGAGGGGCTGGCTGGTCACCAGAGGGTGGGGCGGACCGCT
GCGCTCGGCGGCTGCGGAGAGGGGGAGAGCAGGCAGCGGGCGGCGGGAGCAGCATGGAGCCGGCGGC
GGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCCACGGCCGCGGCCCGGGTGGGTAGAGGAGGT
GCGGGCGCTGCTGGAGGCGGGGGCGCTGCCAACGCACCGAATAGTTACGGTCGGAGGCCGATCCAGGT
GGGTAGAGGGTCTGCAGCGGGAGCAGGGGATGGCGGGCGACTCTGGAGGACGAAGTTTGCAGGGGAATT
GGAATCAGGTAGCGCTTCGATTCTCCGAAAAAGGGGAGGCTTCTGGGGAGTTTTCAGAAGGGGTTTGTA
ATCAGACCTCCTCCTGGCGACGCCCTGGGGCTTGGGAAGCAAGGAAGAGGAATGAGGAGCCACGCG
CGTACAGATCTCTGAATGCTGAGAAGATCTGAAGGGGGGAACATATTTGTATTAGATGGAAGTATGCTCTTT
ATCAGATACAAAATTTACGAACGTTTGGGATAAAAAGGGAGTCTTAAGAAATGTAAGATGTGCTGGGACTAC
TAGCCTCCAATTCACAGATACCTGGATGGAGCTTATCTTTCTTACTAGGAGGGATTATCAGTGGAATCTGT

FIG. 29A

GGTGTATGTTGGAATAAATATCGAATATAAATTTTGATCGAAATTATTCAGAAGCGGCCGGGCGGGTGCCTC
ACGCCTTGTAATCCCTTCACTTTGGGAGATCAAGGCGGGGGAATCACCTGAGGTCGGGAGTTCGAGACCA
GCCTGGCCAACAGGTGAAACCTCGCCTCTACTAAAAATACAAAAAGTAGCCGGGGGTGGTGGCAGGCGCCT
GTAATCCCAGCTACTCGGGAGGTTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCTGAGGTTGTAGTGAAC
AGCGAGATGGAGCCACTTCACTCCAGCCTGGGTGACAGAGTGAGACTTTGTCGAAAGAAAGAAAGAGAGAA
AGAGAGAGAGAAAAATTATTCAGAAGCAACTACATATTGTGTTTATTTTAACTGAGTAGGGCAAATAAATATA
TGTTTGCTGTAGGAACCTAGGAAATAATGAGCCACATTCATGTGATCATTCCAGAGGTAATATGTAGTTACCAT
TTTGGGAATATCTGCTAACATTTTTGCTCTTTTACTATCTTTAGCTTACTTGATATAGTTTATTTGTGATAAGAG
TTTTCAATTCCTCATTTTTGAACAGAGGTGTTTCTCCTCTCCCTACTCCTGTTTTGTGAGGGAGTTAGGGGAG
GATTTAAAAGTAATTAACATGGGTAACCTAGCATCTCTAAATTTTGCCAACAGCTTGAACCCGGGAGTTTG
GCTTTGTAGTCCTACAATATCTTAGAAGAGACCTTATTTGTTTAAAAACAAAAAGGAAAAAGAAAAGTGGATAG
TTTTGACAATTTTAAATGGAG

FIG. 29B

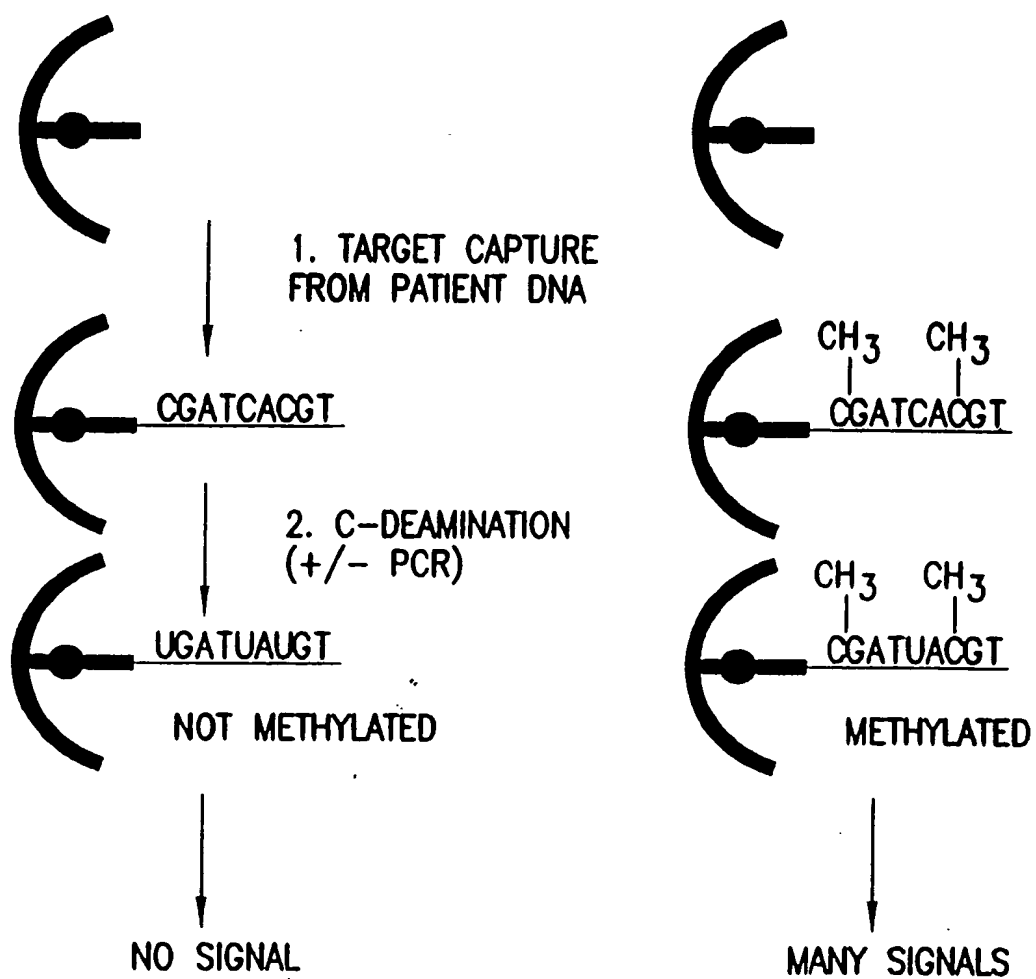


FIG. 30